

SEQUENCE LISTING

<110> Holloway, James L.
Lok, Si

<120> SECRETED PROTEIN ZACRP4

<130> 99-29

<150> 60/141,928

<151> 1999-07-01

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)...(1196)

<400> 1

cgcccgggccc	ctggccccag	caccctgtcc	gctgccgcct	cagagccggg	aaaagcagcc	60
ggagcccccg	ccgcccctgc	cgcagcgcg	gcggtcagcg	cgagccccg	caccgcagc	120
ctgcagcctg	cagcccgcag	cccgcagccc	ggagccagat	cgcgggctca	gaccgaaccc	180
gactcgaccg	ccgccccag	ccaggcgcc	atg ctg ccg	ctt ctg ctg	ggc ctg	233
			Met Leu Pro	Leu Leu Leu	Gly Leu	
			1	5		

ctg ggc cca	gcg gcc tgc	tgg gcc ctg	ggc ccg acc	ccc ggc ccg	gga	281
Leu Gly Pro	Ala Ala Cys	Trp Ala Leu	Gly Pro Thr	Pro Gly Pro	Gly	
10	15		20			

tcc tct gag	ctg cgc tcg	gcc ttc tcg	gcg gca cgc	acc acc ccc	ctg	329
Ser Ser Glu	Leu Arg Ser	Ala Phe Ser	Ala Ala Arg	Thr Thr Pro	Leu	
25	30		35		40	

gag ggc acg	tcg gag atg	gcg gtg acc	ttc gac aag	gtg tac gtg	aac	377
Glu Gly Thr	Ser Glu Met	Ala Val Thr	Phe Asp Lys	Val Tyr Val	Asn	

45	50	55	
atc ggg ggc gac ttc gat gtg gcc acc ggc cag ttt cgc tgc cgc gtg Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg Val 60 65 70			425
ccc ggc gcc tac ttc ttc tcc ttc acg gct ggc aag gcc ccg cac aag Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His Lys 75 80 85			473
agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag gtg cag gcg ctg Ser Leu Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala Leu 90 95 100			521
gcc ttc gac gag cag cgg cgg cca ggc gcg cgg cgc gca gcc agc cag Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser Gln 105 110 115 120			569
agc gcc atg ctg cag ctc gac tac ggc gac aca gtg tgg ctg cgg ctg Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu 125 130 135			617
cat ggc gcc ccg cac tac gcg cta ggc gcg ccc ggc gcc acc ttc agc His Gly Ala Pro His Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser 140 145 150			665
ggc tac cta gtc tac gcc gac gcc gac gct gac gcg cct gcg cgc ggg Gly Tyr Leu Val Tyr Ala Asp Ala Asp Ala Pro Ala Arg Gly 155 160 165			713
ccg ccc gcg ccc ccc gag ccg cgc tcg gcc ttc tcg gcg gcg cgc acg Pro Pro Ala Pro Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr 170 175 180			761
cgc agc ttg gtg ggc tcg gac gct ggc ccc ggg ccg cgg cac caa cca Arg Ser Leu Val Gly Ser Asp Ala Gly Pro Gly Pro Arg His Gln Pro 185 190 195 200			809
ctc gcc ttc gac acc gag ttc gtc aac att ggc ggc gac ttc gac gcg Leu Ala Phe Asp Thr Glu Phe Val Asn Ile Gly Gly Asp Phe Asp Ala 205 210 215			857
gcg gcc ggc gtg ttc cgc tgc cgt ctg ccc ggc gcc tac ttc ttc tcc Ala Ala Gly Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser 220 225 230			905

ttc acg ctg ggc aag ctg ccg cgt aag acg ctg tcg gtt aag ctg atg 953
 Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met
 235 240 245

aag aac cgc gac gag gtg cag gcc atg att tac gac gac ggc gcg tcg 1001
 Lys Asn Arg Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser
 250 255 260

cgg cgc cgc gag atg cag agc cag agc gtg atg ctg gcc ctg cgg cgc 1049
 Arg Arg Arg Glu Met Gln Ser Gln Ser Val Met Leu Ala Leu Arg Arg
 265 270 275 280

ggc gac gcc gtc tgg ctg ctc agc cac gac cac gac ggc tac ggc gcc 1097
 Gly Asp Ala Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala
 285 290 295

tac agc aac cac ggc aag tac atc acc ttc tcc ggc ttc ctg gtg tac 1145
 Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr
 300 305 310

ccc gac ctc gcc ccc gcc gcc ccg ccg ggc ctc ggg gcc tcg gag cta 1193
 Pro Asp Leu Ala Pro Ala Ala Pro Pro Gly Leu Gly Ala Ser Glu Leu
 315 320 325

ctg tgagccccgg gccagagaag agcccgggag ggccaggggc gtgcatgcc 1246
 Leu

ggccggggccc gaggtcgaa agtcccgcgc gagcgccacg gcctccgggc gcgcctggac 1306
 tctgccaata aagcggaaag cgggcacgcg cagcgcccgg cagcccaggc a 1357

<210> 2

<211> 329

<212> PRT

<213> Homo sapiens

<400> 2

Met Leu Pro Leu Leu Leu Gly Leu Leu Gly Pro Ala Ala Cys Trp Ala
 1 5 10 15
 Leu Gly Pro Thr Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe
 20 25 30
 Ser Ala Ala Arg Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val
 35 40 45
 Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala
 50 55 60

Thr Gly Gln Phe Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe
 65 70 75 80
 Thr Ala Gly Lys Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg
 85 90 95
 Asn Arg Asp Glu Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro
 100 105 110
 Gly Ala Arg Arg Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr
 115 120 125
 Gly Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu
 130 135 140
 Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala
 145 150 155 160
 Asp Ala Asp Ala Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg
 165 170 175
 Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala
 180 185 190
 Gly Pro Gly Pro Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val
 195 200 205
 Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg
 210 215 220
 Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg
 225 230 235 240
 Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala
 245 250 255
 Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln
 260 265 270
 Ser Val Met Leu Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser
 275 280 285
 His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile
 290 295 300
 Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Pro Ala Ala Pro
 305 310 315 320
 Pro Gly Leu Gly Ala Ser Glu Leu Leu
 325

<210> 3
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Clq Aromatic Motif

<221> VARIANT
 <222> (2)...(6)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan or
leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (26)...(26)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (28)...(28)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (30)...(30)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (31)...(31)

<223> Xaa is phenylalanine or tyrosine

<400> 3

Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Tyr	Xaa	Phe	Xaa	Xaa		
			20				25					30			

<210> 4
 <211> 987
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide sequence encoding the
 polypeptide of SEQ ID NO:2

<221> variation
 <222> (1)...(987)
 <223> Each N is A, T, G or C

<400> 4

atgytnccny	tnytnytngg	nytnytnggn	ccngcngcnt	gytgggcnyt	nggnccnacr	60
ccnggnccng	gnwsnwsnga	rytnmgnwsn	gcnttywsng	cngcnmgnac	nacnccnytn	120
garggnacnw	sngaratggc	ngtnacntty	gayaargtnt	aygtnaayat	hggnggngay	180
ttygaygtng	cnacnggnca	rttymgtngy	mgngtnccng	gngcntaytt	ytywsntty	240
acngcnggna	argcncnca	yaarwsnytn	wsngtnatgy	tngtnmgnaa	ymnggaygar	300
gtncargcny	tngcnttyga	ygarcarmgn	mgncnccngg	cnmgnmgngc	ngcnwsncar	360
wsngcnatgy	tnrcarytnga	ytayggngay	acngtntggg	tnmgnytnca	ygngcncnccn	420
caytaygcny	tnggngcncc	nggngcnacr	ttywsnggnt	ayytngtnta	ygcngaygcn	480
gaycngayg	cncngcnmg	nggnccnccn	gcncnccng	arccnmgnws	ngcnttywsn	540
gcngcnmgna	cnmgnwsnyt	ngtnggnwsn	gaycnggnc	cnggnccnmg	ncaycarccn	600
ytngcnttyg	ayacngartt	ygtnaayath	ggnggngayt	tygaygcngc	ngcnggngtn	660
ttymgtngym	gnytnccngg	ngcntaytty	ttywsnttya	cnytnggnaa	rytnccnmgn	720
aaracnytnw	sngtnaaryt	natgaaraay	mgngaygarg	tnrcargcnat	gathtaygay	780
gayggngcnw	snmgnmgngm	ngaratgcar	wsncarwsng	tnatgytngc	nytnmgnmgn	840
ggngaygcng	tntggytnyt	nwsncaygay	caygayggnt	ayggngcnta	ywsnaaycay	900
ggnaartaya	thacnttyws	nggnttyytn	gtntayccng	ayytngcncc	ngcngcncnccn	960
ccnggnytn	gngcnwsnga	rytnytn				987

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC20,839

<400> 5

atgtacttgc cgtggttgct gtag

24

<210> 6

<211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC20840

<400> 6
 cgacaccgag ttcgtcaaca ttg 23

<210> 7
 <211> 325
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide sequence encoding the
 polypeptide of SEQ ID NO:2.

<221> variation
 <222> (1)...(325)
 <223> Each N is independently A, T, C or G.

<400> 7
 ctggccccgg gccgcggcac caaccactcg ccttcgacac cgagttcgtc aacattggcg 60
 gcgaattcga cgcggcggcc ggcgtgttcc gctgccgtct gnccggcgcc tactttctct 120
 nttcacgct gggcaagctg ccgcgtaaga cgctgtcggt taagctgatg aagaaccgcg 180
 acgaggtgca ggccatgatt tacgacgacg gcgcgtcgcg gcgccgag atgcagagcc 240
 agagcgtgat gctggccctg cggcgcgng acgccgtctg gctgtcagcc acgaccacga 300
 cggctacggc gcctacagca accac 325

<210> 8
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC22162

<400> 8
 ccgcggcacc aaccactc 18

<210> 9
 <211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC 22168

<400> 9

gtcgcggttc ttcattcag

18

gtcgcggttc ttcattcag